



1	soMGD	Α	MSHPSTVTSEPSN-LLDFVPKLGNFVLNSSLHGNNSNGYSSFSSNSVHFGGLATQN	55
}	csMGD	A	MRNPSTVVQENGS-VSDFISQLGYFAFSSRFLNLNSEGCSGSSSHSLYLNGFENYRCVKR	59
•	atMGD	A	MQNPSTVTQESAAPVFDFFPRLRGLTSRNRSPCSNSDGYALSSSNALYFNGFRTLPS-RR	59
	atMGD	В		0
	soMGD	A	RYKFVNSLSFSKEGSNLKRILSDFNRVIRLHCDRI-PLGFSSIGLNSGESNGVSD	109
	csMGD		PPRSGASLSLSSRGSSSLRRFVNEFNNVIKFHCHKP-PLGFASLGGVSDETNGIRD	
	atMGD		MGKTLASLSFNTKSSAGSSLRRFISDFNSFIRFHCDKVVPESFASVGGVGLSSDENGIRE	
	atMGD		MATTVMALAEKVLERVYGTSKSAVSVTSGDGEKTHRHTHHHIHRIKSYDDIDE	
			::	
	soMGD	A	NGHG-VLEDVRVPVNAVEPESPKRVLILMSDTGGGHRASAEAIKAAFNEEFGDDYQVFVT	168
	csMGD	A	DGFG-VSQDGALPLNKIEAENPKRVLILMSDTGGGHRASAEAIKAAFNEEFGNNYQVFIT	173
	atMGD	A	NGTGGVLGEEGLPLNGVEADRPKKVLILMSDTGGGHRASAEAIRAAFNQEFGDEYQVFIT	179
	atMGD	В	DESSLELIQIGAERTKNVLILMSDTGGGHRASAEAIRDAFKIEFGDKYRVIVK	106
			: : : : : : : : : : : : : : : : : : :	
			h1	
	soMGD		DLWSEHTPWPFNQLPRSYNFLVKHGPLWKMMYYGTSPRVIHQSNFAATSVFIAREVARGL	
	csMGD		DLWTDHTPWPFNQLPRSYNFLVKHGTLWKMTYYVTAPKVIHQSNFAATSTFIAREVAKGL	
	atMGD		DLWTDHTPWPFNQLPRSYNFLVKHGTLWKMTYYGTSPRIVHQSNFAATSTFIAREIAQGL	
	atMGD	В	DVWKEYTGWPLNDMERSYKFMVKHVQLWKVAFHSTSPKWIHSCYLAAIAAYYAKEVEAGL	166
			::::* **:*: ***:*: ***: ***: :: *::: :*:: :*:: : *::: : : *::: : : : : : : : : : : : : : : : : : :	
		_	h2*	000
	soMGD		MKYQPDIIISVHPLMQHVPLRILRGRGLLEKIVFTTVVTDLSTCHPTWFHKLVTRCYCPS	
	csMGD		MKYRPDIIISVHPLMQHVPIRILRSKGLLNKIVFTTVVTDLSTCHPTWFHKLVTRCYCPS	
	atMGD atMGD		MKYQPDIIISVHPLMQHVPLRVLRSKGLLKKIVFTTVITDLSTCHPTWFHKLVTRCYCPS MEYKPEIIISVHPLMOHIPLWVLKWOELOKRVLFVTVITDLNTCHPTWFHPGVNRCYCPS	
	achgb	ь	*: *: *: ** ** ** * * * : : : : : : : :	220
	soMGD	Δ	NEVAKRATKAGLQPSQIKVYGLPVRPSFVRSVRPKNELRKELGMDEHLPAVLLMGGGEGM	348
	csMGD		TEVAKRALTAGLOPSKLKVFGLPVRPSFVKPIRPKIELRKELGMDENLPAVLLMGGGEGM	
	atMGD		TEVAKRAQKAGLETSQIKVYGLPVRPSFVKPVRPKVELRRELGMDENLPAVLLMGGGEGM	
	atMGD		QEVAKRALFDGLDESQVRVFGLPVRPSFARAVLVKDDLRKELEMDQDLRAVLLMGGGEGM	
			***** **: *:::*:*******:::: * :*::* **::* *****	
			h3* h4	
;	soMGD	A	GPIEATARALGNALYDANLGEPTGQLLVICGRNKKLAGKLSSIDWKIPVQVKGFVTKIEE	408
	csMGD	A	GPIEATAKALSKALYDENHGEPIGQVLVICGHNKKLAGRLRSIDWKVPVQVKGFVTKMEE	413
i	atMGD	A	GPIEATARALADALYDKNLGEAVGQVLIICGRNKKLQSKLSSLDWKIPVQVKGFITKMEE	419
i	atMGD	В	GPVKETAKALEEFLYDKENRKPIGQMVVICGRNKKLASALEAIDWKIPVKVRGFETQMEK	346
			** <u>:: **:** : ***</u> : :: **:::***:*** : * ::***:**:* <u>* *::*:</u>	
			h5*	
	soMGD		CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGQEAGNVPYVIENGIGKYLKSPKEIA 4	
	csMGD		CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGQEAGNVPYVVENGCGKFSKSPKEIA 4	
	atMGD		CMGACDCIITKAGPGTIAEAMIRGLPIILNGYIAGQEAGNVPYVVENGCGKFSKSPKEIS 4	
ě	atMGD	В	WMGACDCIITKAGPGTIAESLIRSLPIILNDYIPGQEKGNVPYVVENGAGVFTRSPKETA 4	106

		_	h6*	
	SOMGD		KTVSQWFGPKANELQIMSQNALKHARPDAVFKIVHDLDELVRQKIFVRQYSCAA 5	
	SMGD		NIVAKWFGPKADELLIMSQNALRLARPDAVFKIVHDLHELVKQRSFVPQYSG 5	
	atMGD		KIVADWFGPASKELEIMSQNALRLAKPEAVFKIVHDMHELVRKKNSLPQLSCTA 5	
ē	atMGD	R	RIVGEWFSTKTDELEQTSDNARKLAQPEAVFDIVKDIDELSEQRGPLASVSYNLTSSFASLV	468
			: *::**:: ::**	





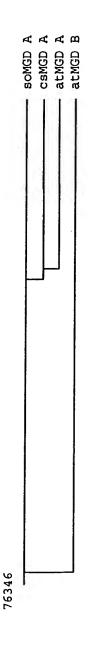


FIG. 2B



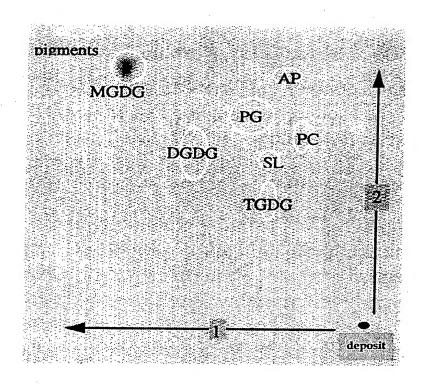


FIG. 3A



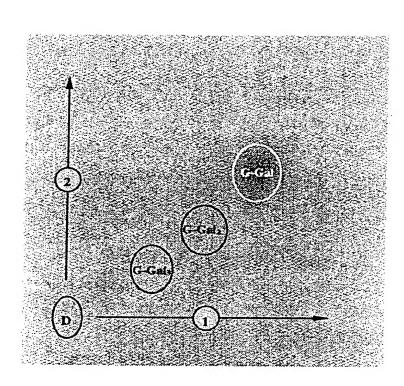


FIG. 3B



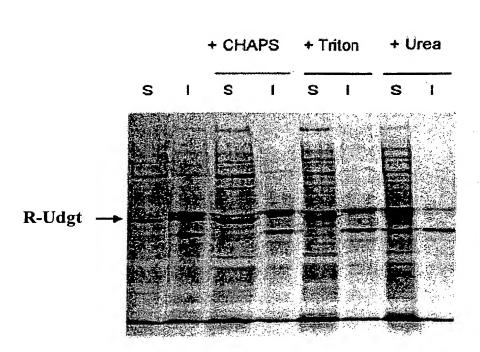


FIG. 4



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FIG. 5A

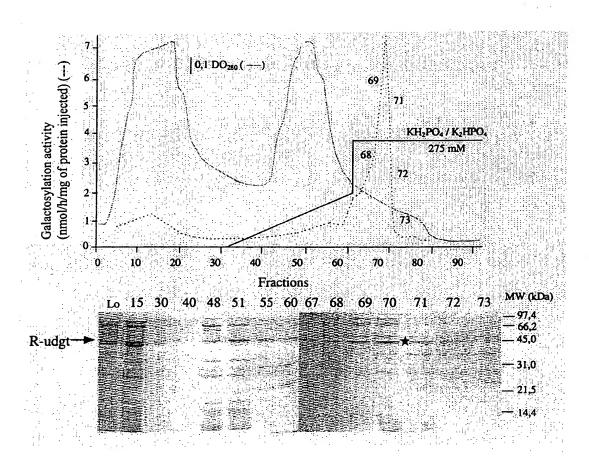


FIG. 5B